MF\_transferase activity
MF\_ATP binding
MF\_nucleotide binding
BP\_protein transport
BP\_transport
MF\_bydrolase activity
MF\_metal ion binding
MF\_DNA binding
BP\_regulation of transcription, DNA-templated
BP\_transcription, DNA-templated
MF\_RNA binding
BP\_oxidation-reduction process
MF\_oxidoreductase activity
BP\_metabolic process
MF\_catalytic activity
BP\_proteopysis
MF\_cappidase activity
BP\_proteopysis
MF\_peptidase activity
BP\_nucleic acid phosphodiester bond hydrolysis BP\_nucleic acid phosphodiester bond hydrolysis BP\_nucleic acid phosphodiester bond hydrolysis MF\_nuclease activity
BP\_transposition, RNA-mediated
BP\_RNA phosphodiester bond hydrolysis
BP\_RNA phosphodiester bond hydrolysis, endon
BP\_DNA biosynthetic process
MF\_DNA-drected DNA polymerase activity
MF\_aspartic-type endopeptidase activity
MF\_sapartic-type endopeptidase activity
BP\_RNA-dependent DNA biosynthetic process
MF\_RNA-DNA hybrid fibonuclease activity
BP\_DNA internation BP\_DNA integration
MF\_RNA-directed DNA polymerase activity MF\_RNA-directed DNA polymerase activity BP\_transposition MF\_ribonuclease activity BP\_DNA recombination MF\_nucleotid/transferase activity BP\_DNA recombination MF\_nucleotid/transferase activity BP\_phosphorylation MF\_sinase activity BP\_protein phosphorylation MF\_protein sense activity BP\_translation MF\_protein sense activity BP\_translation MF\_protein sense through the protein sense -BP\_call cycle
BP\_call division
MF\_zinc ion binding
BP\_positive regulation of transcription by RNA polymerase II
BP\_call cycle
BP\_call division
MF\_zinc ion binding
BP\_positive regulation of transcription by RNA polymerase II
BP\_transcription by RNA polymerase II
MF\_sequence-specific DNA binding
BP\_rinkla processing
MF\_nucleic acid binding
MF\_mRNA binding
BP\_mRNA processing
BP\_mRNA processing
BP\_mRNA splicing, via spliceosome
BP\_RNA splicing, via spliceosome
BP\_RNA splicing
BP\_mRNA splicing
BP\_mRNA splicing
BP\_mRNA splicing
BP\_mRNA splicing
BP\_callular response to DNA damage stimulus
BP\_DNA repair
BP\_visite—mediated transport
BP\_ENE of Colly vesicle—mediated transport
BP\_EN Carboyld vesicle—mediated transport
BP\_ion transport
MF\_transporter activity
MF\_transportactivity
BP\_carboyld-rate transport
BP\_amino acid transport
BP\_amino acid transport
BP\_amino acid transport
BP\_amino acid transport
BP\_moundering transcription factor activity, RNA polymerase II—specific
MF\_DNA-binding transcription factor activity, RNA polymerase II—specific
MF\_proximal promoter DNA-binding transcription activator activity, RNA polymerase II—specific
MF\_proximal promoter formal promoter sequence—specific DNA binding
BP\_cagative regulation of transcription by RNA polymerase II
BP\_regulation of transcription by RNA polymerase 4 \_\_ Ę Æ <u>,</u> Ę In F., helicase activity

MF\_Alfases activity

MF\_Alfases activity

MF\_Alfases activity

BP\_lipid metabolic process

BP\_methylation

MF\_methylation

MF\_methylation

MF\_methylation

MF\_methylation

BP\_entocylosis

BP\_positive regulation of GTPase activity

MF\_GTPase activator activity

BP\_Dositive regulation of GTPase activity

MF\_GTPases activator activity

BP\_macroautophagy

BP\_autophagy of mitochondrion

BP\_piecemeal microautophagy of the nucleus

BP\_autophagy of mitochondrion

BP\_protein incalization by the Cvt pathway

BP\_protein inport into nucleus

MF\_protein in  $\subseteq$ 로파움을 참 선지 집기 BP\_cellular response to oxidative stress
BP\_protein binding
MF\_unfolded protein binding
MF\_unfolded protein binding
MF\_unfolded protein binding
MF\_transferase activity, transferring acyl groups
BP\_cautohydrate metabolic process
MF\_tyrdroses activity, acting on glycosyl bonds
BP\_DNA duplax unwinding
MF\_ATP-dependent RNA helicase activity
BP\_maturation of LSU-4RNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
BP\_ribosomal large subunit assembly
MF\_rRNA binding
BP\_maturation of SSU-4RNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
BP\_endonucleolytic cleavage in TSTS to spearate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
BP\_endonucleolytic cleavage in TSTS to spearate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
BP\_endonucleolytic cleavage in TSTS to strictstonic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
BP\_endonucleolytic cleavage in SSU-rRNA from 5.8S rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
BP\_chromosome segregation
MF\_protein binding
MF\_protein binding binding
BP\_preprotein binding binding
BP\_preprotein binding binding
MF\_protein binding, bridging
BP\_protein binding, bridging blidging bridging BP\_phospholipid biosynthetic process BP\_exocytosis BP\_mRNA export from nucleus
BP\_poly(A)+ mRNA export from nucleus
BP\_poly(A)+ mRNA export from nucleus
MF\_structural molecule activity
MF\_lipid binding
MF\_phosphatidylinositol-3-phosphate binding
MF\_publiquitin binding
BP\_retrograde wesicle-mediated transport, Golgi to ER
BP\_vacuole fusion, non-autophagic
MF\_SNABEP\_bind
SNABEP\_bind
SNABEP\_bi MF\_SNARE binding BP\_cellular iron ion homeostasis BP\_cellular iron ion homeostasis BP\_iron ion homeostasis MF\_microtubule binding BP\_positive regulation of catalytic activity MF\_histone binding MF\_protein heterodimerization activity BP\_GPI anchor biosynthetic process BP\_triacarboxylic acid cycle BP\_mitochondrial genome maintenance BP\_mitochondrial genome maintenance BP\_mitochondrial genome maintenance BP\_mitochondrion organization
BP\_response to stress
BP\_cellular response to heat
BP\_regulation of cell size
BP\_actin cytoskeleton organization
BP\_response to pheromone
MF\_IRNA binding
BP\_ribosomal small subunit biogenesis
BP\_RNA processing
MF\_guanyl-nucleotide exchange factor activity
BP\_actin filament organization
MF\_actin binding BP\_actin filament organization
MF\_actin binding
BP\_chromatin silencing at silent mating-type cassette
BP\_chromatin silencing at telomere
BP\_chromatin silencing at telomere
BP\_telomere maintenance
BP\_telomere maintenance
BP\_telomere maintenance via recombination
BP\_double-strand break repair
BP\_nucleotide-excision repair
BP\_ucleotide-Maintenance BP\_nucleotide-excision repair
MF\_damaged DNA binding
BP\_DNA replication initiation
MF\_DNA replication ringin binding
MF\_double-stranded DNA binding
MF\_single-stranded DNA binding
MF\_single-stranded DNA binding
BP\_dephosphorylation
BP\_protein dephosphorylation
MF\_phosphorylation
MF\_phosphorylation
MF\_pinspingle-meiotic recombination
MF\_single-stranded DNA binding
MF\_single-stranded
MF\_single MF\_isomerase activity
MF\_magnesium in on binding
BP\_aerobic respiration
BP\_proton transmembrane transport
MF\_iron-sulfur cutser binding
BP\_cell redox homeostasis
MF\_electron transfer activity
BP\_DNA replication
MF\_chromatin binding
BP\_positive requisition of transcription MF\_chromatin binding
BP\_positive regulation of transcription elongation from RNA polymerase II promoter
BP\_transcription elongation from RNA polymerase II promoter
MF\_DNA translocase activity
BP\_chromatin remodeling
BP\_RNA polymerase II preinitiation complex assembly
BP\_chromatin organization
BP\_histone acetylation
MF\_histone acetylation
MF\_bistone acetylation for activity
BP\_pointiation elotylation for activity
BP\_pointiation resulting in formation of a cellular spore
BP\_sportulation ┖ BP\_mitochondrial translation MF\_GTP binding MF\_GTPase activity

3.0

0.6

0.4

0.2